

S5 Table. Nucleotide sequence alignments of clones selected with sera pool.

Clone	Freq.	Identity - blastN	GeneBank No.	% identity	start	end
HB_RRG7	1/42	HS amyloid beta precursor protein (APP)	NM_201413.2	95	1037	1298
HB_RRF1	1/42	HS ATP synthase, H ⁺ transporting, mitochondrial Fo complex subunit E (ATP5I)	NM_007100.3	0	87	240
HB_RRB7	1/42	HS brain expressed X-linked 2 (BEX2)	NM_001168399.1	100	444	700
HB_RRH5	1/42	HS DEAD-box helicase 24 (DDX24)	NM_020414.3	100	357	744
HB_RRC8	1/42	HS DEAD-box helicase 24 (DDX24)	NM_020414.3	99	392	658
HB_RRH11	1/42	HS heterogeneous nuclear ribonucleoprotein U like 2 (HNRNPUL2)	NM_001079559.2	100	2214	2379
HB_RRH2	1/42	HS microtubule associated protein 1B (MAP1B)	NM_005909.4	100	2189	2523
HB_RRB8	1/42	HS adenylate kinase 5 (AK5)	NM_174858.2	100	1897	1719
HB_RRE2	1/42	HS RNA, 28S ribosomal (LOC109910382), ribosomal RNA	NR_146154.1	97	1861	2009
HB_RRC3	1/42	HS cystathionine-beta-synthase (CBS)	NM_000071.2	100	1622	1854
HB_RRA12	1/42	HS hypoxia up-regulated 1 (HYOU1), transcript variant 2	NM_001130991.2	100	3998	3580
HB_RRA11	1/42	HS RANBP2-like and GRIP domain containing 5 (RGPD5)	NM_005054.2	100	3487	3470
HB_RRC6 ^a	1/42	HS protein phosphatase 4 regulatory subunit 4 (PPP4R4)	NM_058237.1	100	3113	2891
HB_RRH9 ^a	6/42	n.a	n.a			
HB_RRB10 ^b	20/42	HS GRB10 interacting GYF protein 2 (GIGYF2)	NM_001103147.1	99	2628	2976
HB_RRD12 ^b	3/42	HS DExH-box helicase 9 (DHX9)	NM_001357.4	100	3720	3975

BlastN analysis of 42 positive clones identified by the selection of phage display cDNA library from human brain with pooled and purified IgG from sera of MS patients. For the meaning of column heading see the legend of S3 Table.

^aout of frame clones

^bbackground clones shared with the anti-human IgG selection